



## SEQUENCE LISTING

<110> LORZ, HORST  
LUTTICKE, STEPHANIE  
ABEL, GERNOT  
GENSCHEL, ULRICH

<120> NUCLEIC ACID MOLECULES WHICH CODE FOR ENZYMES  
DERIVED FROM WHEAT AND WHICH ARE INVOLVED IN  
THE SYNTHESIS OF STARCH

<130> 514413-3849.1

<140> 09/674,817

<141> 2000-11-06

<150> WO 99/58690

<151> 1999-11-18

<150> DE 198 20 608.9

<151> 1998-05-08

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<170> PatentIn version 3.3

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Met	Asn	Arg	Thr	Gly	Asn	Val	Trp	His	Val	Phe	Ile	Glu	Gly	Glu	Leu	
	110					115					120					
cag	gac	atg	ctt	tac	ggg	tac	agg	ttc	gac	ggc	acc	ttt	gct	cct	cac	435
Gln	Asp	Met	Leu	Tyr	Gly	Tyr	Arg	Phe	Asp	Gly	Thr	Phe	Ala	Pro	His	
125					130					135					140	
tgc	ggg	cac	tac	ctt	gat	gtt	tcc	aat	gtc	gtg	gtg	gat	cct	tat	gct	483
Cys	Gly	His	Tyr	Leu	Asp	Val	Ser	Asn	Val	Val	Val	Asp	Pro	Tyr	Ala	
			145						150					155		
aag	gca	gtg	ata	agc	cga	ggg	gag	tat	ggg	gtt	ccg	gcg	cgt	ggg	aac	531
Lys	Ala	Val	Ile	Ser	Arg	Gly	Glu	Tyr	Gly	Val	Pro	Ala	Arg	Gly	Asn	
		160					165					170				
aat	tgc	tgg	cct	cag	atg	gct	ggc	atg	atc	cct	ctt	cca	tat	agc	acg	579
Asn	Cys	Trp	Pro	Gln	Met	Ala	Gly	Met	Ile	Pro	Leu	Pro	Tyr	Ser	Thr	
		175					180					185				
ttt	gat	tgg	gaa	ggc	gac	cta	cct	cta	aga	tat	cct	caa	aag	gac	ctg	627
Phe	Asp	Trp	Glu	Gly	Asp	Leu	Pro	Leu	Arg	Tyr	Pro	Gln	Lys	Asp	Leu	
	190					195					200					
gta	ata	tat	gag	atg	cac	ttg	cgt	gga	ttc	acg	aag	cat	gat	tca	agc	675
Val	Ile	Tyr	Glu	Met	His	Leu	Arg	Gly	Phe	Thr	Lys	His	Asp	Ser	Ser	
205					210					215					220	
aat	gta	gaa	cat	ccc	ggg	act	ttc	att	ggg	gct	gtg	tcg	aag	ctt	gac	723
Asn	Val	Glu	His	Pro	Gly	Thr	Phe	Ile	Gly	Ala	Val	Ser	Lys	Leu	Asp	
				225					230					235		
tat	ttg	aag	gag	ctt	gga	gtt	aat	tgt	att	gag	tta	atg	ccc	tgc	cat	771
Tyr	Leu	Lys	Glu	Leu	Gly	Val	Asn	Cys	Ile	Glu	Leu	Met	Pro	Cys	His	
		240						245					250			
gag	ttc	aac	gag	ctg	gag	tac	tca	acc	tct	tct	tcc	aag	atg	aac	ttt	819
Glu	Phe	Asn	Glu	Leu	Glu	Tyr	Ser	Thr	Ser	Ser	Ser	Lys	Met	Asn	Phe	
		255					260					265				
tgg	gga	tat	tct	acc	ata	aac	ttc	ttt	tca	cca	atg	acg	aga	tac	aca	867
Trp	Gly	Tyr	Ser	Thr	Ile	Asn	Phe	Phe	Ser	Pro	Met	Thr	Arg	Tyr	Thr	
	270					275					280					
tca	ggc	ggg	ata	aaa	aac	tgt	ggg	cgt	gat	gcc	ata	aat	gag	ttc	aaa	915
Ser	Gly	Gly	Ile	Lys	Asn	Cys	Gly	Arg	Asp	Ala	Ile	Asn	Glu	Phe	Lys	
285					290					295					300	

act ttt gta aga gag gct cac aaa cgg gga att gag gtg atc ctg gat	963
Thr Phe Val Arg Glu Ala His Lys Arg Gly Ile Glu Val Ile Leu Asp	
305 310 315	
gtt gtc ttc aac cat aca gct gag ggt aat gag aat ggt cca ata tta	1011
Val Val Phe Asn His Thr Ala Glu Gly Asn Glu Asn Gly Pro Ile Leu	
320 325 330	
tca ttt agg ggg gtc gat aat act aca tac tat atg ctt gca ccc aag	1059
Ser Phe Arg Gly Val Asp Asn Thr Thr Tyr Tyr Met Leu Ala Pro Lys	
335 340 345	
gga gag ttt tat aac tat tct ggc tgt ggg aat acc ttc aac tgt aat	1107
Gly Glu Phe Tyr Asn Tyr Ser Gly Cys Gly Asn Thr Phe Asn Cys Asn	
350 355 360	
cat cct gtg gtt cgt caa ttc att gta gat tgt tta aga tac tgg gtg	1155
His Pro Val Val Arg Gln Phe Ile Val Asp Cys Leu Arg Tyr Trp Val	
365 370 375 380	
acg gaa atg cat gtt gat ggt ttt cgt ttt gat ctt gca tcc ata atg	1203
Thr Glu Met His Val Asp Gly Phe Arg Phe Asp Leu Ala Ser Ile Met	
385 390 395	
acc aga ggt tcc agt ctg tgg gat cca gtt aac gtg tat gga gct cca	1251
Thr Arg Gly Ser Ser Leu Trp Asp Pro Val Asn Val Tyr Gly Ala Pro	
400 405 410	
ata gaa ggt gac atg atc aca aca ggg aca cct ctt gtt act cca cca	1299
Ile Glu Gly Asp Met Ile Thr Thr Gly Thr Pro Leu Val Thr Pro Pro	
415 420 425	
ctt att gac atg atc agc aat gac cca att ctt gga ggc gtc aag ctc	1347
Leu Ile Asp Met Ile Ser Asn Asp Pro Ile Leu Gly Gly Val Lys Leu	
430 435 440	
gtt gct gaa gca tgg gat gca gga ggc ctc tat caa gta ggt caa ttc	1395
Val Ala Glu Ala Trp Asp Ala Gly Gly Leu Tyr Gln Val Gly Gln Phe	
445 450 455 460	
cct cac tgg aat gtt tgg tct gag tgg aat ggg aag tac cgg gac att	1443
Pro His Trp Asn Val Trp Ser Glu Trp Asn Gly Lys Tyr Arg Asp Ile	
465 470 475	
gtg cgt caa ttc att aaa ggc act gat gga ttt gct ggt ggt ttt gcc	1491
Val Arg Gln Phe Ile Lys Gly Thr Asp Gly Phe Ala Gly Gly Phe Ala	
480 485 490	
gaa tgt ctt tgt gga agt cca cac cta tac cag gca gga gga agg aaa	1539
Glu Cys Leu Cys Gly Ser Pro His Leu Tyr Gln Ala Gly Gly Arg Lys	
495 500 505	
cct tgg cac agt atc aac ttt gta tgt gca cac gat gga ttt aca ctg	1587
Pro Trp His Ser Ile Asn Phe Val Cys Ala His Asp Gly Phe Thr Leu	
510 515 520	

gct gat ttg gta aca tat aat aac aag tac aat tta cca aat ggg gag	1635
Ala Asp Leu Val Thr Tyr Asn Asn Lys Tyr Asn Leu Pro Asn Gly Glu	
525 530 535 540	
aac aac aga gat gga gaa aat cac aat ctt agc tgg aat tgt ggg gag	1683
Asn Asn Arg Asp Gly Glu Asn His Asn Leu Ser Trp Asn Cys Gly Glu	
545 550 555	
gaa gga gaa ttc gca aga ttg tct gtc aaa aga ttg agg aag agg cag	1731
Glu Gly Glu Phe Ala Arg Leu Ser Val Lys Arg Leu Arg Lys Arg Gln	
560 565 570	
atg cgc aat ttc ttt gtt tgt ctc atg gtt tct caa gga gtt cca atg	1779
Met Arg Asn Phe Phe Val Cys Leu Met Val Ser Gln Gly Val Pro Met	
575 580 585	
ttc tac atg ggt gat gaa tat ggc cac aca aaa ggg ggc aac aac aat	1827
Phe Tyr Met Gly Asp Glu Tyr Gly His Thr Lys Gly Gly Asn Asn Asn	
590 595 600	
aca tac tgc cat gat tct tat gtc aat tat ttt cgc tgg gat aaa aaa	1875
Thr Tyr Cys His Asp Ser Tyr Val Asn Tyr Phe Arg Trp Asp Lys Lys	
605 610 615 620	
gaa caa tac tct gac ttg cac cga ttc tgt tgc ctc atg acc aaa ttc	1923
Glu Gln Tyr Ser Asp Leu His Arg Phe Cys Cys Leu Met Thr Lys Phe	
625 630 635	
cgc aag gag tgc gag ggt ctt ggc ctt gag gat ttt cca acg gcc gaa	1971
Arg Lys Glu Cys Glu Gly Leu Gly Leu Glu Asp Phe Pro Thr Ala Glu	
640 645 650	
cgg ctg cag tgg cat ggt cat cag cct ggg aag cct gat tgg tct gag	2019
Arg Leu Gln Trp His Gly His Gln Pro Gly Lys Pro Asp Trp Ser Glu	
655 660 665	
aat agc cga ttc gtt gcc ttt tcc atg aaa gat gaa aga cag ggc gag	2067
Asn Ser Arg Phe Val Ala Phe Ser Met Lys Asp Glu Arg Gln Gly Glu	
670 675 680	
atc tat gtg gcc ttc aac acc agc cac tta ccg gcc gtt gtt gag ctc	2115
Ile Tyr Val Ala Phe Asn Thr Ser His Leu Pro Ala Val Val Glu Leu	
685 690 695 700	
ccg gag cgc aca ggg cgc cgg tgg gaa ccg gtg gtg gac aca ggc aag	2163
Pro Glu Arg Thr Gly Arg Arg Trp Glu Pro Val Val Asp Thr Gly Lys	
705 710 715	
cca gca cca tac gac ttc ctc act gac gac tta cct gat cgc gct ctc	2211
Pro Ala Pro Tyr Asp Phe Leu Thr Asp Asp Leu Pro Asp Arg Ala Leu	
720 725 730	
acc ata cac cag ttc tct cat ttc ctc aac tcc aac ctc tac ccc atg	2259
Thr Ile His Gln Phe Ser His Phe Leu Asn Ser Asn Leu Tyr Pro Met	
735 740 745	

ctc agc tac tca tcg gtc atc cta gta ttg cgc cct gat gtt tga 2304  
 Leu Ser Tyr Ser Ser Val Ile Leu Val Leu Arg Pro Asp Val  
 750 755 760

gaggcggata tacagtaaat aatatgtata tatgtagtcc tttggcgtat tatcagtgtg 2364

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aaaaaaactc gag 2437

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<213> Triticum aestivum L. cv. Florida

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Glu Asp Glu Gly Glu Glu Asp Glu Pro Val Ala Glu Asp Arg Tyr Ala  
 35 40 45

Leu Gly Gly Ala Cys Arg Val Leu Ala Gly Met Pro Thr Pro Leu Gly  
 50 55 60

Ala Thr Ala Leu Ala Gly Gly Val Asn Phe Ala Val Tyr Ser Gly Gly  
 65 70 75 80

Ala Thr Ala Ala Ala Leu Cys Leu Phe Thr Pro Glu Asp Leu Lys Ala  
 85 90 95

Asp Arg Val Thr Glu Glu Val Pro Leu Asp Pro Leu Met Asn Arg Thr  
 100 105 110

Gly Asn Val Trp His Val Phe Ile Glu Gly Glu Leu Gln Asp Met Leu  
 115 120 125

Tyr Gly Tyr Arg Phe Asp Gly Thr Phe Ala Pro His Cys Gly His Tyr  
 130 135 140

Leu Asp Val Ser Asn Val Val Val Asp Pro Tyr Ala Lys Ala Val Ile  
 145 150 155 160

Ser Arg Gly Glu Tyr Gly Val Pro Ala Arg Gly Asn Asn Cys Trp Pro  
 165 170 175

Gln Met Ala Gly Met Ile Pro Leu Pro Tyr Ser Thr Phe Asp Trp Glu  
 180 185 190

Gly Asp Leu Pro Leu Arg Tyr Pro Gln Lys Asp Leu Val Ile Tyr Glu  
 195 200 205

Met His Leu Arg Gly Phe Thr Lys His Asp Ser Ser Asn Val Glu His  
 210 215 220

Pro	Gly	Thr	Phe	Ile	Gly	Ala	Val	Ser	Lys	Leu	Asp	Tyr	Leu	Lys	Glu	225	230	235	240
Leu	Gly	Val	Asn	Cys	Ile	Glu	Leu	Met	Pro	Cys	His	Glu	Phe	Asn	Glu	245	250	255	
Leu	Glu	Tyr	Ser	Thr	Ser	Ser	Ser	Lys	Met	Asn	Phe	Trp	Gly	Tyr	Ser	260	265	270	
Thr	Ile	Asn	Phe	Phe	Ser	Pro	Met	Thr	Arg	Tyr	Thr	Ser	Gly	Gly	Ile	275	280	285	
Lys	Asn	Cys	Gly	Arg	Asp	Ala	Ile	Asn	Glu	Phe	Lys	Thr	Phe	Val	Arg	290	295	300	
Glu	Ala	His	Lys	Arg	Gly	Ile	Glu	Val	Ile	Leu	Asp	Val	Val	Phe	Asn	305	310	315	320
His	Thr	Ala	Glu	Gly	Asn	Glu	Asn	Gly	Pro	Ile	Leu	Ser	Phe	Arg	Gly	325	330	335	
Val	Asp	Asn	Thr	Thr	Tyr	Tyr	Met	Leu	Ala	Pro	Lys	Gly	Glu	Phe	Tyr	340	345	350	
Asn	Tyr	Ser	Gly	Cys	Gly	Asn	Thr	Phe	Asn	Cys	Asn	His	Pro	Val	Val	355	360	365	
Arg	Gln	Phe	Ile	Val	Asp	Cys	Leu	Arg	Tyr	Trp	Val	Thr	Glu	Met	His	370	375	380	
Val	Asp	Gly	Phe	Arg	Phe	Asp	Leu	Ala	Ser	Ile	Met	Thr	Arg	Gly	Ser	385	390	395	400
Ser	Leu	Trp	Asp	Pro	Val	Asn	Val	Tyr	Gly	Ala	Pro	Ile	Glu	Gly	Asp	405	410	415	
Met	Ile	Thr	Thr	Gly	Thr	Pro	Leu	Val	Thr	Pro	Pro	Leu	Ile	Asp	Met	420	425	430	
Ile	Ser	Asn	Asp	Pro	Ile	Leu	Gly	Gly	Val	Lys	Leu	Val	Ala	Glu	Ala	435	440	445	
Trp	Asp	Ala	Gly	Gly	Leu	Tyr	Gln	Val	Gly	Gln	Phe	Pro	His	Trp	Asn	450	455	460	
Val	Trp	Ser	Glu	Trp	Asn	Gly	Lys	Tyr	Arg	Asp	Ile	Val	Arg	Gln	Phe	465	470	475	480
Ile	Lys	Gly	Thr	Asp	Gly	Phe	Ala	Gly	Gly	Phe	Ala	Glu	Cys	Leu	Cys	485	490	495	
Gly	Ser	Pro	His	Leu	Tyr	Gln	Ala	Gly	Gly	Arg	Lys	Pro	Trp	His	Ser	500	505	510	
Ile	Asn	Phe	Val	Cys	Ala	His	Asp	Gly	Phe	Thr	Leu	Ala	Asp	Leu	Val	515	520	525	

Thr Tyr Asn Asn Lys Tyr Asn Leu Pro Asn Gly Glu Asn Asn Arg Asp  
 530 535 540  
 Gly Glu Asn His Asn Leu Ser Trp Asn Cys Gly Glu Glu Gly Glu Phe  
 545 550 555 560  
 Ala Arg Leu Ser Val Lys Arg Leu Arg Lys Arg Gln Met Arg Asn Phe  
 565 570 575  
 Phe Val Cys Leu Met Val Ser Gln Gly Val Pro Met Phe Tyr Met Gly  
 580 585 590  
 Asp Glu Tyr Gly His Thr Lys Gly Gly Asn Asn Asn Thr Tyr Cys His  
 595 600 605  
 Asp Ser Tyr Val Asn Tyr Phe Arg Trp Asp Lys Lys Glu Gln Tyr Ser  
 610 615 620  
 Asp Leu His Arg Phe Cys Cys Leu Met Thr Lys Phe Arg Lys Glu Cys  
 625 630 635 640  
 Glu Gly Leu Gly Leu Glu Asp Phe Pro Thr Ala Glu Arg Leu Gln Trp  
 645 650 655  
 His Gly His Gln Pro Gly Lys Pro Asp Trp Ser Glu Asn Ser Arg Phe  
 660 665 670  
 Val Ala Phe Ser Met Lys Asp Glu Arg Gln Gly Glu Ile Tyr Val Ala  
 675 680 685  
 Phe Asn Thr Ser His Leu Pro Ala Val Val Glu Leu Pro Glu Arg Thr  
 690 695 700  
 Gly Arg Arg Trp Glu Pro Val Val Asp Thr Gly Lys Pro Ala Pro Tyr  
 705 710 715 720  
 Asp Phe Leu Thr Asp Asp Leu Pro Asp Arg Ala Leu Thr Ile His Gln  
 725 730 735  
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 Ser Val Ile Leu Val Leu Arg Pro Asp Val  
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33